



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : <b>C12N 15/31, C07K 14/22, 16/12, C12Q 1/68, A61K 39/095, G01N 33/50</b>		A2	(11) International Publication Number: <b>WO 99/57280</b> (43) International Publication Date: 11 November 1999 (11.11.99)																								
(21) International Application Number: <b>PCT/US99/09346</b>		(US). MASIGNANI, Vega [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). MORA, Marirosa [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). PETERSEN, Jeremy [US/US]; Arlington, VA (US). PIZZA, Mariagratia [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RAPPOLI, Rino [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). RATTI, Giulio [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCALATO, Enzo [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). SCARSELLI, Maria [IT/IT]; Chiron S.p.A., Via Fiorentina, 1, I-53100 Siena (IT). TETTELIN, Herve [US/US]; Gaithersburg, MD (US). VENTER, J., Craig [US/US]; Rockville, MD (US).																									
(22) International Filing Date: 30 April 1999 (30.04.99)		(74) Agent: HARBIN, Alisa, A.; Chiron Corporation, Intellectual Property – R440, P.O. Box 8097, Emeryville, CA 94662-8097 (US).																									
(30) Priority Data: <table> <tr><td>60/083,758</td><td>1 May 1998 (01.05.98)</td><td>US</td></tr> <tr><td>60/094,869</td><td>31 July 1998 (31.07.98)</td><td>US</td></tr> <tr><td>60/098,994</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr> <tr><td>60/099,062</td><td>2 September 1998 (02.09.98)</td><td>US</td></tr> <tr><td>60/103,749</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/103,794</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/103,796</td><td>9 October 1998 (09.10.98)</td><td>US</td></tr> <tr><td>60/121,528</td><td>25 February 1999 (25.02.99)</td><td>US</td></tr> </table>		60/083,758	1 May 1998 (01.05.98)	US	60/094,869	31 July 1998 (31.07.98)	US	60/098,994	2 September 1998 (02.09.98)	US	60/099,062	2 September 1998 (02.09.98)	US	60/103,749	9 October 1998 (09.10.98)	US	60/103,794	9 October 1998 (09.10.98)	US	60/103,796	9 October 1998 (09.10.98)	US	60/121,528	25 February 1999 (25.02.99)	US	(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).	
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(71) Applicants (for all designated States except US): CHIRON CORPORATION [US/US]; 4560 Horton Street, Emeryville, CA 94608 (US). THE INSTITUTE FOR GENOMIC RESEARCH [US/US]; 9212 Medical Center Drive, Rockville, MD 20850 (US).		<p><b>Published</b>  <i>Without international search report and to be republished upon receipt of that report.</i></p>																									
(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS																											
(57) Abstract <p>The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.</p> <p style="text-align: right;"><b>919 (46 kDa)</b></p>																											
<p style="text-align: right;"><b>A) PURIFICATION</b></p> <p style="text-align: right;">M1 919</p>																											

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DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

a147.seq

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1 ATGCGACGAG AAGCCAAAAT GGCACAAACT ACACCTCAAAC CCATTGTTT
51 ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAAGCG CATGGAACGT
101 AGCAATCAGT GGGCTTGGAA ACGGTCAAGCG TCGTCGGCAA AAGCCGTCCG
151 CGGCCCACTT CGGGCTGCT GCACACTTCT ACCGCCTCCG ACAAAATCAT
201 CAGCGGCGAC ACCTTGCAC AAAAAGCCGT CAACCTGGGT GATGCTTAG
251 ACGGCGTACC GGGCATTCTAT GCCTCGCAAT ACGGGCGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGGGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTCGAA CAGGTGCAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGACAG GCTCGGGAA TGTGGCGGGG CTGGTCGATG TTGCGGATGG
501 CAAAATCCCC GAAAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGCCTTGAG CAGCGGCAAT CTGGAAAAAC TCACGTCGGG CGGCATCAAT
601 ATCGGTTTGG GCAAAACATT TGTATTGCAAC ACGGAAGGGC TGTAACCGCAA
651 ATCGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTCGAA ACGGGCAGCG TCGGGCTGTC TTGGGTTGGC
751 GAAAAGGCT TTATCGGCG AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGCAAAAGAG TTTGATTAAC AAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACCTC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGGCG ATGCACTGAG AAACCTTTTT ACAACACCAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCATAA TTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAC
1301 ATTACAGCTT TTTCGGTGTA GAACAGGCAA ACTGGGACAA CTTCACGCTT
1351 GAAGGCGGGC TACCGTGGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACCG CCAAACCGCC CGCTCATTG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAAACT CAGCCTGACC GCCTCCCATC AGGAACGCC
1551 GCCGTCAACG CAAGAGCTGT ACGCACACGG CAAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGCGC TGGGCTACGA AGGCAGCCGC TGGCAATACA ATCTGGCACT
1701 CTACCGAAC CGCTTCGGCA ACTACATTCA CGCCCAAAAC TTAAACGACG
1751 GACCGGGCCC CAAATCCATC GAAGACGACA CGAATGAA GCTCGTGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTTACCG GCATCGGCGT TTCCGGCGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACCGCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCGTCCGGC
2001 TGCGCGCTC GGCCTCCACC TGAAAGCTC GCTGACCGAC CGCATCGATG
2051 CCAATTGGA CTACTACCGC GTGTTCGCCC AAAACAAACT CGCCCGCTAC
2101 GAAACCGACA CGCCCGGACA CCATATGCTC AACCTCGCG CAAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGGAAATG GTACGTCAAAC GCGACAAAC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCGC
2251 CAAATGGGCC CGAGCTTACCG CGGCGCGTGC AACGTGAAGT TTTAA

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This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

a147.pep

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1 MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51 RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIKGQTGRR IKVLNHHGET GDMADFSRPH AIMVDSALSQ QVEILRGPV
151 LLYSSGNVAG LVDVADGKIP EKMPENGVSG ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNLIK RLPDSHADSDQ TGSIGLSWVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWOKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLRLNKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTQNARIE LRHQPIGRKL
401 GSWGVQYLGQ KSSALSATSE AVKQPMLLDN KVQHYSFFGV EQANWDNFTL
451 EGGVRVEKQK ASIRYDKALI DRENYYNHPL PDLGKAHRQTA RSFALSGNWY
501 FTPQHKLSTL ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

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1101 AGGTCGTCTG AAAGGCAGCT GGGCGTGCA ATATTTACAA CAAAAATCCA  
 1151 GTGCTTATC TGCCATATCC GAAGCGGTTA AACAAACCGAT GCTGCTTGAC  
 1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA  
 1251 CAACTTCACG CTTGAAGGAG GCGTACCGGT GGAAAACAA AAAGCCTCCA  
 1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC  
 1351 CTGCCCGACC TCGGCACGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC  
 1401 GGGCAACTGG TATTTCACGC CACAACACAA ACTCAGCCTG ACCGCCTCCC  
 1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC  
 1501 GTGCCACCA ACACCTTGA AGTCGGCAAC AAACACCTCA ACAAAAGAGCG  
 1551 TTCCAACAAAT ATCGAACCTG CGCTGGGCTA CGAAGGGCGAC CGCTGGCAAT  
 1601 ACAAATCTGC ACTCTACCGC AACCGCTTCG GTAACTACAT TTACGCCAA  
 1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT  
 1701 GAAGCTCGTG CGCTACAAACC AATCGGCGC CGACTTCTAC GGCGCGGAAG  
 1751 GCGAAATCTA CTTCAAACCG AACCGCGCT ACCGCATCGG CGTTTCCGGC  
 1801 GACTATGTAC GAGGCCGTCT GAAAAACCTG CCTTCCTAC CGGGCAGAGA  
 1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCC  
 1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC  
 1951 GACCGTATCG ATGCCAATTT GGACTACTAC CGCGTGTTCG CCCAAACAA  
 2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCAACCTCG  
 2051 GCGCAAACTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC  
 2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACCA GCAGCTTTCT  
 2151 CTCTGATAACG CCGCAAATGG GCCGCAGCTT TACCGCGGGC GTGAACGTGA  
 2201 AGTTTTAA

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

**m147.pep** (partial)

1	..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51	GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMADFS
101	HAIMVDTALS QQVEILRGPV TLYSSGNVA GLVDVADGKI PEKMPENGVS
151	GELGLRLSSG NLEKLTSIGGI NIGLGKNFVL HTEGLYRKSG DYAVPRYRN
201	KRLPDSHADS QTGSIGLSWV GEKGFIGVAY SDRRDQYGLP AHSHEYDDCH
251	ADIWIWQKSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301	GRPWIIDLRSK RYELRAEWKQ PFPFGFEALRV HLNRNDYRHD EKAGDAVENF
351	FNNQTQNARI ELRHQPIGRL KGSWGVQYILO QKSSALSAIS EAVKQPM
401	NKVQHYSFFG VEQANWDNFT LEGGVRVKEQ KASIQYDKAL IDRENYYNHP
451	LPDLGAHRQT ARSFALSGNW YFTPQHKLSL TASHQERLPS TQELYAHGKH
501	VATNTFEVGN KHLNKERSNN IELALGYEGD RWQYNLALYR NRFGNYIYAQ
551	TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIYFKP TPRYRIGVSG
601	DYVRGRKLKNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAAR LGFHLKASLT
651	DRIDANLDYY RVFAQNKLAR YETRTPGHM LNMGANYRRN TRYGEWNWYV
701	KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

**m147 / g147** 92.3% identity in 142 aa overlap

m147.pep						
PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS						
:      :      :      :      :      :						
g147	MRREAKMAQITLKPIVL SILLINTPLLAQAHETEQSVGLET VSVVGKSR PRATSGLLHTS					
	10	20	30	40	50	60
m147.pep	TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAP VIRGQTGRRIKVLNHHGET					
	40	50	60	70	80	90
g147	TASDKIISGDTLRQKAVNLGDALDGVPGI HASQYGGGASAP VIRGQTGRRIKVLNHHGET					
	70	80	90	100	110	120
m147.pep	GDMADFS PDHAIMVDTALSQQVEILRGPV TLYSSGNVAGLVDVADGKI PEKMPENGVSG					
	100	110	120	130	140	150
g147	GDMADFS PDHAIMVDTALSQQVEILRGPV TLYSSGNVAGAGQCCRWNPKNA					

601 YNQSGADFYG AEGEIYFKPT PRYRIGVSGD YVRGRLKNLP SLPGREDAYG  
 651 NRPLIAQADQ NAPRVPAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY  
 701 ETRTPGHHML NLGANRYRRNT RYGEWNWYVK ADNLINQSVY AHSSFLSDTP  
 751 QMGRSFTGGV NVKE\*

m147/a147 98.1% identity in 734 aa overlap

		10	20	30	
m147.pep		PHKTEQSVDLET	VS	VGKSRPRAT	SGLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQAHGTEQSVGLET				
		10	20	30	40
		40	50	60	70
m147.pep	TASDKIISGDTLQRKAVNLGDALDGVPGIHASQYGGGASAP	80	90	100	110
a147	VIRGQTGRRIKVLNHHGET	120			
		70	80	90	100
m147.pep	GDMADFS PDHAIMVDTALSQQVEILRGPVTL	130	140	150	160
a147	LYSSGNVAGLVDVADGKIP	170	180	190	200
		130	140	150	160
m147.pep	ELGLRLSSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYA	210	220	230	240
a147	VPRYRNLKRLPDSHADSQ	250	260	270	280
		190	200	210	220
m147.pep	TGSIGLSWVGEKGFIGVAYS	290	300	310	320
a147	SDRRDQYGLPAHSHEYDDCHADI	300	310	320	330
		250	260	270	280
m147.pep	LTEEDIDYDNPGLSCGFHD	340	350	360	370
a147	DDNAHAHTHSGRPWIDL	380	390	400	410
		370	380	390	400
m147.pep	NRNDYRHDEKAGDAVENF	420	430	440	450
a147	NQNTOQNARIELRHQPI	440	450	460	470
		430	440	450	460
m147.pep	PDLGAHRQTARS	480	490	500	510
a147	FALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKH	500	510	520	530
		490	500	510	520
m147.pep	HLNKERSNNIELALGYEGDRWQYNLALYRNRF	540	550	560	570
a147	QNYIYAQTLNDGRGP	550	560	570	580
		520	530	540	550

	550	560	570	580	590	600
m147.pep	580	590	600	610	620	630
	YNQSGADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQ					
a147	610	620	630	640	650	660
	YNQSGADFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQ					
m147.pep	640	650	660	670	680	690
	NAPRVPAA RLGFHLKASLT DRIDANLD YYRVFA QNK LARYE TRTPGH HMLNL GANY RRNT					
a147	670	680	690	700	710	720
	NAPRVPAA RLGVHLKASLT DRIDANLD YYRVFA QNK LARYE TRTPGH HMLNL GANY RRNT					
m147.pep	700	710	720	730		
	RYGEWNWYVKADNLLNQS VYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	730	740	750	760		
	RYGEWNWYVKADNLLNQS VYAHSSFLSDTPQMGRSFTGGVNVKFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

g148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGctgg	ttcaTCCCGA
51	AgctATgagt	gtccgcgCgc	TTGccgAcaa	AATCCGCAAA	AtcgaAAact
101	gGCCGCAAAA	AGgcataCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGT
151	GCGGAATACT	TCCGCCTTTT	GGTCGATTTG	CTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGCTTGGG	CGCCGCGGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTTACCAAG	CTCAaCGtcg	gctTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTGA	AACCGTATCG	CAAAGCTAcg	cgcTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	tgcgcgTCAAA	CCCGGTTCGC
401	GCGTCTTGACT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	AATGCTTGCC
451	GGGCTGGAAC	TGATCCGCAA	ACTCGGGGG	GAAATTGTCG	AAggcgccgC
501	CATTTGGAA	TTTACCGACC	TTCAAGGGGG	CAAGAATATC	CGCGCAAGTG
551	GCGCGCCCTT	ATTTACCCCTG	CTTCAAAACG	AAGGCTGCAT	GAAAGGCTGA

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

g148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDOKI	DIVAGLDARG	FIIGAALAYQ	LNVGFVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	PGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

m148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTGGCGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTTCAAAGC
151	GCGGAATACT	TCCGCCTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGG	CGCCGCGGGC	TTCATTATCG
251	GCGCGGCACT	CGCCTTACCAAG	CTCACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAA	CTCGGTTCGC
401	GCGTCTTGACT	GGTCGATGAT	TTGATTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGACTGGAAC	TGATCCGCAA	ACTCGGGGG	GAAATTGTCG	AAggcgccgC
501	CATTTGGAA	TTTACCGACC	TTCAAGGGGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTTACCCCTG	CTTCAAAACG	AAGGCTGTAT	GAAAGGCTGA

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

m148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDOKI	DIVAGLDARG	FIIGAALAYQ	LNVGFVPIRK

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSGWVQ  
 401 YLGQKSSALS AIPETVQQPM LIIDNNVRHYS FFGVEQANWD NFTLEGGVRY  
 451 EKQKASIRYD KALIDRENYY NQPLPDGLAH RQTARSFALS GNWYFTPQHK  
 501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY  
 551 EGDRWQYNLA AYRNRFGNYI YAQLNDGRG PKSIEDDSEM KLVRYNQSGA  
 601 DFYGAEGEYY FKPTPRYRIG VSGDYVRGRRL KNLPSLPGRE DPYGKRPFIA  
 651 QADQNAPRIP AARLGFLKLT SLTDRIDANL DYRRVFAQNK LARYETRTPG  
 701 HHMLNLGANR RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
 751 TGGVNVKF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

**m149-1.seq**

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATT CTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGATTG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCCCTC CGACAAAATC ATCTCGGGG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CGGGGCATCC
251 ACGCTTCGCA ATACGGCGC GGCACGTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGGCAGGC GGATTAAGT GTGAAACAT CACGGCGAAA CAGGCAGATAT
351 GGCAGATTTC TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTGCG
401 AACAGGTGCA AATCTGCGC GGGCCGGTTA CGCTCTTGTG CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TTGTCGGAT GCGAAAATCC CCGAAAAAAAT
501 GCCTGAAAAC GGCATGTCG GCGAACCTCGG ATTGCGTTG AGCAGCGGCA
551 ATCTGGAAA ACTCACGTCC GGCAGGATCA ATATCGGTTT GGGCAAAAAC
601 TTTGATTGCA ACACGGAAAG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACGCGTGTAC CGCAATCTGA AACGCCCTGCG CGACAGCCAC GCCGATTGCG
701 AAACGGGAG CATCGGGCTG TCTTGGGTTG GCGAAAAAGG TTTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCG CCCACAGCCA
801 CGAACATCGAT GATTGCCACG CGCACATCAT CTGGCAAAG AGCTTGATTA
851 ACAAAACGCTA TTTACAGCTT TATCCGCACC TGTTGACCGA AGAACACATC
901 GATTGACGAA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CCCTGCCGAA TGAAGCAAC CGTCCCCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAGCAGG
1101 CGATGCAGTC GAAAACCTTT TTAACAAACCA AACGCAAAAC GCCCGCATCG
1151 ATTTGCGCCA CAAACCCATA GGTGCTCTGA AAGGCAGCTG GGGCGTGC
1201 TATTTAACAC AAAATCCAG TGCTTTATCT GCCATATCG AAGCGTTAA
1251 ACAACCGATG CTGCTGACA ACAAAAGTGCA ACATTACAGC TTTTCGGTG
1301 TAGAACAGGC AAAACTGGGAC AACTTCACGC TTGAAGGAGG CGTACCGTG
1351 GAAAACACAA AAGCCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGG
1401 AAACACTTAC AACACCCCCC TGCCCGACCT CGGCGCGCAC CGGCAACACG
1451 CCCGCTCATC CGCACCTTCG GGCACACTGGT ATTTACGCG ACAACACAAA
1501 CTCAGCCTGA CGCCTCCCA TCAGGAACGC CTGCGCTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAAACAGC TCGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAAATA TCAGACTCGC GCTGGGCTAC
1651 GAAGGGCAGC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTG GCTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAAACCGA CACCGGGCTA
1851 CGGCATCGC GTTCCCGGCG ACTATCTACG AGGCCGTCG AAAAACCTGC
1901 CTTCCTTACCC CGCGCAGAGAA GATGCCATCG GCAACCGTCC TTTCATCGCA
1951 CAGGACGACCC AAAATGCCCG CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CAAAAACAAA CTCGCCCCTG ACGAAACCGG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACACTAC CGCGCAATA CGCGCTATGG
2151 CGAGTGGAAAT TGGTACGTCA AAGCCGACAA CCTGCTAAC CAATCCGTTT
2201 ACGCCACACAG CAGCTTCTC TCTGATACGC CGCAAATGGG CGCGAGCTTT
2251 ACCGGCGGCG TGAACGTGAA GTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

**m149-1.pep**

```

1 MAQTTLKP ILSILLINTPL LAQAHETEQS VDLETVSVVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIVDVT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGELGLRL SSGNLEKLTS GGINIGLGN
201 FVLHTEGLYR KSGDYAVPRY RNKLRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSDRRDQY GLPAHSHEYD DCHADIWQK SLINKRQLQ YPHLLTEEDI
301 DYDNPGGLSCG FHDDDNAHAA THSGRPWIDL RNKRYELRAE WKQPFPGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTNQ ARIELRHQPI GRLKGSGWVQ
401 YLQQKSSALS AISEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRY
451 EKQKASIRYD KALIDRENYY NHPLPDGLAH RQTARSFALS GNWYFTPQHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

```

a149		PAARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANRNRNTRYGEW				
	250	260	270	280	290	300
m149.pep	310	320	330	340		
a149		NWYVKADNLLNQSVDYAHSSFLSDTPQMGRSFTGGVNFKFX				
	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 601>:

**g149-1.seq**

```

1 ATGGCACAAA TCACACTCAA ACCCATTGTT TTATCAATT CTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGGCAC TTGGGGCTG
151 CTGCACACTT CGACCGCCTC CGACAAAATC ATCTCGGCG ATACTTTGG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTTT GGACGGCGTA CGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GGCGCATCCG CTCCCGTTAT TCGGGTCAA
301 ACGGGCAGAC GGATTAAGT ATTGAACCAT CACGGCGAAA CGGGCGATAT
351 GGCAGACTT TCTCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTGCG
401 AACAGGTGAA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGC
451 AATGTGGCGG GGCTGGTCGA TGTTGCCGAT GGAAAAATCC CCGAAAAAAAT
501 GCCTGAAAAC GGCGTATCGG CGGaagccgg ATTGCGTTTG AGCAGCGGCA
551 ATTTAGAAAA ACTGACATCC CGAGGCATCA ATATCGGACT GGGCAAAAC
601 TTCGTGCTGC ATACCGAAGG CTGGTACCGC AAATCGGGCG ATTACGCCGT
651 ACCGCCTTAC CGCAATCTGA AACGCCCTGC CGACAGCCAT GCCGATTGCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTGG CGGAAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCGCTAC GGCGTCCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATCA
851 ACAAAACGCTA TTTGAGCTT TATCCGACT TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGCTT GAGCTGCGGC TTCCACGACG GCGACGGTGC
951 ACACGACAC ACCCACAAACG GCAAACCGTG GATAGACCTG CGAACAAAC
1001 GCTACGAACCT CGCGCCGAA TGGAAAGCAGC CATTCCCCGG TTTTGAAGCC
1051 CTGCGCGTAC ATCTGAACCG CAATGACTAC CACCACGAGC AAAAAGCAGG
1101 CGATGCACTA GAAAACCTCT TCAACAAACAA AACACACAAAC GCCCCTATCG
1151 AGTTGCGCCA CCAACCCATA GGCGCTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTGGGAC AAAAATCCAG CGCGCTTTCC GCGATTCCCG AAACCGTCCA
1251 ACAACCGATG TTGATTGACA ACAATGTCCG CCATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAATTTGGGAC AACTTCACGC TTGAAGGGGG CGTACCGGTG
1351 GAAAACAAA AAGCCTCCAT CGGGTACGAC AAAGCATTGA TTGATCGAGA
1401 AAAACTACTAC AACACGCCCG TGCCCGGACCT CGCGCGGCAC CGCCAAACCG
1451 CCCGCTCGTT CGCACTTTCG GGCAACTGCTG ATTCACGCC ACACCAACAA
1501 CTCAGCCTGA CGCCTCCCA TCAGGAACGC CTGCGTCAA CGCAAGAACT
1551 GTACGACACG GGCAAGCACG TCGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGGCACC GCTGGCAATA CAATCTGGCA GCCTACCGCA ACCGATTGCG
1701 CAACTACATT TACGCCAAA CCTTAAACGA CGGACGGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAAACCA ATCCGGTGC
1801 GACTTCTACG CGCGGGAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CGGCATCGGT GTTTCGGCG ACTATGTACG AGGCGCTCTG AAAAACCTGC
1901 CGTCCCTTAC CGGCAGGGAA GATCCCTACG GCAAACGTCC CTTCATCGCA
1951 CAAGCCGACC AAAACGCCCG CGCATTCCCG GCTGCGGCC TCGGCTTCCA
2001 CCTGAAAACC TCGCTAACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCGCT ACGAAACCGG TAGGCCCGGA
2101 CACCATATGC TCAACCTCGG TGCAAACATAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAAT TGGTACGTCA AAGCCGACAA CCTGCTAAC CAATCGTTT
2201 ACGCCCCAACAG CAGCTTCCCTC TCTGTACCGC CGCAAATGGG CGCAGCTTT
2251 ACCGGCGGC TAAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 602; ORF 149-1.ng>:

**g149-1.pep**

```

1 MAQITLKPIV LSILLINTPL LAQAHETEQS VGLETVSVVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLDALDGV PGIHASQYGG GASAPVIRGO
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIKEKMPEN GVSGEAGRLI SSGNLEKLTS AGINIGLGN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDRDRY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPGISCG FHDGDGAHAH THNGKPWIDL RNKRYELRAE WKQPFPGFEA

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551 EGDRWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
 601 DFYGAEGEIY FKPTPRYRIG VSGDYVRGRL KNLPLSPGRE DAYGNRPFIA  
 651 QDDQNAPRVP AARLGFLKA SLTDRIDANL DYRVFAQN LARYETRTPG  
 701 HHMLNLGANY RRNTRYGEWN WVKADNLLN QSVYAHSSFL SDTPQMGRSF  
 751 TGGVNVKF\*

m149-1/g149-1 96.2% identity in 758 aa overlap

	10	20	30	40	50	60
m149-1.pep	MAQTTLKPIVLSILLINTPLLAQAHETEQSVDETVSVVGKSRPRATSGLLHTSTASDKI					
g149-1	MAQITLKPIVLSILLINTPLLAQAHETEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI	10	20	30	40	50
	70	80	90	100	110	120
m149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHGETGDMADF					
g149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHGETGDMADF	70	80	90	100	110
	130	140	150	160	170	180
m149-1.pep	SPDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPKEKMPENGVSSELGLRL					
g149-1	SPDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPKEKMPENGVSSEAGLRL	130	140	150	160	170
	190	200	210	220	230	240
m149-1.pep	SSGNLEKLTSGGINIGLGNFKVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL					
g149-1	SSGNLEKLTSAGINIGLGNFKVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL	190	200	210	220	230
	250	260	270	280	290	300
m149-1.pep	SWVGEKGFIGVAYSDRRDQYGLPAHSHEYDDCHADIWQKSLINKRKYQLYPHLTEEDI					
g149-1	SWVGEKGFIGAAYSDRRDYGLPAHSHEYDDCHADIWQKSLINKRKYQLYPHLTEEDI	250	260	270	280	290
	310	320	330	340	350	360
m149-1.pep	DYDNPGLSCGFHDDDNAHAHTHSGRPWIQLRNKRYELRAEWKQPFPGEALRVHLNNDY					
g149-1	DYDNPGLSCGFHDGDGAHAHTHNGKPWIDLRLNKRYELRAEWKQPFPGEALRVHLNNDY	310	320	330	340	350
	370	380	390	400	410	420
m149-1.pep	RHDEKAGDAVENFFNNQTQNARIELRHQPIGRLKGSGWVQYLQQKSSALSAISEAVKQPM					
g149-1	HHDEKAGDAVENFFNNKTHNARIELRHQPIGRLKGSGWVQYLQKSSALSAIPETVQQPM	370	380	390	400	410
	430	440	450	460	470	480
m149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDHALIDRENYYNHPLPDLGAH					
g149-1	LIDNNVRHYSFFGVEQANWDNFTLEGGVRVEKQKASIYDHALIDRENYYNQPLPDLGAH	430	440	450	460	470
	490	500	510	520	530	540
m149-1.pep	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
g149-1	RQTARSFALSGNWYFTPQHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER	490	500	510	520	530
	550	560	570	580	590	600
m149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSGA					
g149-1	SNNIELALGYEGDRWQYNLAAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEMKLVRYNQSGA	550	560	570	580	590
	610	620	630	640	650	660
m149-1.pep	DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP					
g149-1	DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDPYGKRPFIAQADQNAPRIP	610	620	630	640	650

	670	680	690	700	710	720
m149-1.pep	AARLGFLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN        :       :       :       :       :       :       :       :					
g149-1	AARLGFLKTSLDRIDANLDYYRVFAQNKLARYETRTPGHMLNLGANYRRNTRYGEWN 670        680        690        700        710        720					
	730	740	750	759		
m149-1.pep	WYVKADNLLNQSVAHSSFLSDTPQMGRSFTGGVNVKFX        :       :       :       :       :       :					
g149-1	WYVKADNLLNQSVAHSSFLSDTPQMGRSFTGGVNVKFX 730        740        750					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

a149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATT C TTTTAATCAA
51 CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 AAAAAAAAGCC GTCAACTTGG GTGATGCTTT AGACGGCGTA CGGGGCATTG
251 ATGCCCTCGCA ATACGGCGGC GGCGCATCGG CTCCCGTTAT TCAGGGTCAA
301 ACAGGCAGAC GGATTAAGT GTGAACCAT CACGGCGAAA CGGGCGACAT
351 GGCAGACTTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTGCG
401 AACAGGTCGA AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCGA TGTTGGCGAT GGCAAAATCC CCGAAAAAAAT
501 GCCTGAAACGGC GGCTGATCGG GCGAACCTGG ATTGCGTTTG AGCAGGGCA
551 ATCTGGAAAA ACTCACGTC GGCGGCATCA ATATCGGTTT GGGCAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCGT
651 ACCCGGTTAC CGCAATCTGA AACGCGTGC CGACAGCCAC GCCGATTGCG
701 AAACGGGCAG CATCGGGCTG TCTTGGGTTG GCGAAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGAACCGTGC CGACAAATAT GGCTGCGCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CGCACATCAT CTGGCAAAAG AGTTGATTA
851 ACAAAACGCTA TTTCAGCTT TATCCGCACC TGTTGACCGA AGAAAGACATC
901 GATTAGACA ATCCGGGCTT GAGCTGCGGC TTTCAGGACG ACGATGATGC
951 ACACGCCATGCCACAAG CGAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTACGAACT CGCGCCGAA TGGAAGCAAC CGTTCCCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAAACCG CAACGACTAC CGCCACGAGC AAAAAGCAGG
1101 CGATGCAGTA GAAAACTTTT TTAACAAACCA AACGCAAAAC GCCCCTATCG
1151 AGTTGCGCCA CCAACCCATA GGCCTGCTGA AAGGCAGCTG GGGCGTGC
1201 TATTGGGAC AAAAATCTG TGCTTTATCT GCCACATCGG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCAC ATATTACAGC TTTTTCGGT
1301 TAGAACAGGC AAAACTGGGAC AACTTCACGC TTGAAGCGG CGTACGCGTG
1351 GAAAACAAA AAGCCTCCAT CCGCTACGAC AAAGCATGAA TTGATCGGG
1401 AAAACTACTAC ACCATCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTTAC CGCAACTTTCG GGCAACTGGT ATTTCACGCC ACAACACAAA
1501 CTCAGCTGA CCCGACCCCA TCAGGAACCG CTGCCGTCAA CGCAAGAGCT
1551 GTACGCAACAC GGCAAAACACG TGCCACCAA CACCTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGGGCACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCAAA CCTTAAACGCA CGGACCGGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATC AGACTCGTC GCTACAACCA ATCCGGTGG
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAACCCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGGGAA GACGCCCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGGCCGACC AAAACGCCCG TCGCGTCCCG GCTGGCGGCC TCGGGGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCCGCT ACGAAACCGC CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACCTAC CGCCCAATA CGCGCTATGG
2151 CGAGTGGAAAT TGGTACGTCA AAGCCGACAA CCTGCTAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCCTC TCTGATACGC CGCAAATGGG CGCGAGCTTT
2251 ACCGGCGGCG TGAACGTGAA GTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

a149-1.pep

```

1 MAQTTLKPIV LSILLINTPL LSOAHGTEQS VGLETVSVVG KSRPRATSGL
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRRIKVNLH HGETGDMADF SPDHAIVMDS ALSQQVEILR GPVTILYSSG
151 NVAGLVVDAD GKIPKEKMPEN GVSGELGLRL SSGNLEKLTG GGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 AAYSDRDRDQY GLPAHSHEYD DCHADIWQK SLINKRYLQL YPHLITEEDI
301 DYDNPGLSCG FHDDDDAHAH AHNGKPWIDL RNKRYELRAE WKQPFPGFEA

```

351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTQN ARIELRHQPI GRLKGSGWGVQ  
 401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV  
 451 EKQKASIRYD KALIDRENYY NHPLPDGLAH RQTARSFALS GNWYFTPQHK  
 501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY  
 551 EGDRWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
 601 DFYGAEGEIIY FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA  
 651 QADQNAPRVP AARLGVHLKA SLTDRIDANL DYYRVAQNK LARYETRTPG  
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF  
 751 TGGVNVKF\*

a149-1/m149-1 98.0% identity in 758 aa overlap

	10	20	30	40	50	60
a149-1.pep	MAQTTLKPIVLSILLINTPLLSQAHQTEQSVDLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1	MAQTTLKPIVLSILLINTPLLAQAHETEQSVDLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
a149-1.pep	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTRRIKVVLNHHGETGDMADF					
m149-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTRRIKVVLNHHGETGDMADF	70	80	90	100	110
	70	80	90	100	110	120
a149-1.pep	SPDHAIMVDSALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPFKMPENGVSSELGLRL					
m149-1	SPDHAIMVDTALSQQVEILRGPVTLLYSSGNVAGLVDVADGKIPFKMPENGVSSELGLRL	130	140	150	160	170
	130	140	150	160	170	180
a149-1.pep	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL					
m149-1	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNLKRLPDSHADSQTGSIGL	190	200	210	220	230
	190	200	210	220	230	240
a149-1.pep	SWVGEKGFIGAAYSDRRDQYGLPAHSHEYDDCHADIIWQKSLINKRQLQYPHLLTEEDI					
m149-1	SWVGEKGFIGVAYSDRRDQYGLPAHSHEYDDCHADIIWQKSLINKRQLQYPHLLTEEDI	250	260	270	280	290
	250	260	270	280	290	300
a149-1.pep	DYDPNGLSCGFHDDDAHAHANGKPWIQLRKRYELRAEWKQPFPGFEALRVHLNNDY					
m149-1	DYDPNGLSCGFHDDNAHAHTHSGRPWIQLRKRYELRAEWKQPFPGFEALRVHLNNDY	310	320	330	340	350
	310	320	330	340	350	360
a149-1.pep	RHDEKAGDAVENFFNNQTQNARIELRHQPIGRLKGSGWVQYLGQKSSALSATSEAVKQPM					
m149-1	RHDEKAGDAVENFFNNQTQNARIELRHQPIGRLKGSGWVQYLGQKSSALSATSEAVKQPM	370	380	390	400	410
	370	380	390	400	410	420
a149-1.pep	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVKEKQKASIRYDKALIDRENYYNHPLPDGLAH					
m149-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVKEKQKASIRYDKALIDRENYYNHPLPDGLAH	430	440	450	460	470
	430	440	450	460	470	480
a149-1.pep	RQTARSFALSGNWYFTPQHKSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER					
m149-1	RQTARSFALSGNWYFTPQHKSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKER	490	500	510	520	530
	490	500	510	520	530	540
a149-1.pep	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA					
m149-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQSGA	550	560	570	580	590
	550	560	570	580	590	600
	610	620	630	640	650	660

a149-1.pep	DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
m149-1	DFYGAEGEIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP
	610 620 630 640 650 660
a149-1.pep	670 680 690 700 710 720
m149-1	AARLGVLHKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
	670 680 690 700 710 720
a149-1.pep	730 740 750 759
m149-1	WYVKADNLLNQSVAHSSFLSDTPQMGRSFTGGVNVKFX
	730 740 750

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

g150.seq (partial)

```

1 .. TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGCCA ATCAGAAAAT
51 CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGAA
101 GCGGTTCGGA TTTGCACTAC CTCCCCGGCG ACGCGCTCGG CGTTTGGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCAGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAA AACCCCTGCCG GTTGCCTCCG
251 CACTGTTATC CCATTCGAA CTCACGCAA ACACCCCCGC CTTTGTCAAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCAACCGTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTGATT TCCTCGTCG AGGCAGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCCTTC GAACACGAAG
551 GGCAGCGCCAG GGCAGCGCCG GCATCGGGTT TCTTGGCGA CGGCGTGGAA
601 GAGGACGGCA CGGTGGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGCTCC GGTACCGGGCG
701 TCGCACCGTT CCGCGCTTC GTCCAACAAAC GTGCCGCAGA AAATGCGGAA
751 GGCAGAAAATC GGCTGATTTT CGGCAATCCG CATTGGCCG CGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCAG
951 GCATATCTAT GTGTGGCGC ATGCGGCAA AATGGCAAA GAAGTGGAAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCAG GGCATTCCGA CGAAGACGGC
1051 GCAGAAGGAT ATTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA
1101 TTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

g150.pep (partial)

```

1 .. YCKADPFPAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51 DNDPALVGEI LDLLGINPAT EIQQAGGKTLV VASALLSHFE LTQNTPAFK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPAK LTAEQFAGLL
151 RPLAPRILYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFLPED SRKPIVMIGS GTGVAPFRAF VQQRAAENAE
251 GRNWLIIFGNP HFAADFPLYQT EWQQFAKDFL LHRYDFAWSR DQEEKIYVQD
301 KIREQAEGLW QWLQEGAHIY VCGDAAKMAK EVEAALLDVI IGAGHSDEDG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

m150.seq

```

1 ATGCAGAACAA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCACGCA
51 GCTCCCTGTCG GGGCTGGACG CGGCACAATG GGCGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCAGCAGA ACCTTTTCC GTAACCGTCC TTTCCGCCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGGC GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGCGAACG CGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCAGA CCGCCGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAAACTCC AATTGCGCGT ACTGGGTTG

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